



# SEQUENCE LISTING

<110> Nelson B. Freimer  
Hong Chen  
Victor I. Reus  
Susan K. Service  
Lynne Alison McInnes  
Pedro Leon  
Lodewijk Sandkuijl

<120> Method and Compositions for Diagnosing and Treating Chromosome-18p  
Related Disorders

<130> UCAL-154CIP5

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gttcttagct cactgaagcc tcaaattcct gggttcaagt gaccctcca cctcagcccc	240
atgaggacct gggactacag gacacagcta aatccctgac acgg atg aaa att aaa	296
Met Lys Ile Lys	

gca gag aaa aac gaa ggt cct tcc aga agc tgg tgg caa ctt cac tgg	344
Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His Trp	
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Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu Val	
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Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro Thr	
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Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser Glu	
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gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg act ggt	536
Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr Gly	
70 75 80	
att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa cac acc	584
Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His Thr	
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aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag gag gcc	632
Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala	
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ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa gaa agg	680
Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu Arg	
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cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg tct tgc	728
Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys	
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Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser Trp	
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cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca gaa tta His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr Glu Leu 360 365 370			1400
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gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt cca agg Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val Pro Arg 425 430 435			1592
att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg aca gac Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met Thr Asp 440 445 450			1640
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Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys			
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Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu			
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Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser			
275 280 285			
Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys			
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Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly			
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325 330 335			
Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln			
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Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu  
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 His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln  
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 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu  
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gttcatagct cactgaagcc tcaaattcct gggttcaagt gaccctccta cctcagcccc	240
atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc	288
Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu	
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Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Ser Ala	
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ccc act tgg aag gac aaa agt gct atc agt gaa aac ctg aag agt ttt	384
Pro Thr Trp Lys Asp Lys Ser Ala Ile Ser Glu Asn Leu Lys Ser Phe	
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Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu	
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act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gca	480
Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Ala	
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Pro Arg Ile Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg	
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gaa gaa aag cag gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat	624

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Leu	Glu	Glu	Glu	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser	Trp	
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ggt	gaa	tgc	agg	tct	tgc	ctg	gaa	aat	aac	tgc	atg	aga	att	tat	aca	720
Gly	Glu	Cys	Arg	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr	Thr	
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Thr	Cys	Gln	Pro	Ser	Trp	Ser	Ser	Val	Lys	Asn	Lys	Ile	Glu	Arg	Phe	
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Phe	Arg	Lys	Ile	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	
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aaa	gat	ctc	ccc	atc	agt	gaa	aag	ctc	att	gag	gaa	gat	gca	caa	ttg	864
Lys	Asp	Leu	Pro	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	
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Phe	Ser	Val	Ser	Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	
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Gly	Glu	Leu	Asp	Gln	Asn	Leu	Ser	Arg	Cys	Phe	Lys	Phe	His	Glu	Lys	
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435	440	445	
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Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp			
465	470	475	
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Asp	Thr	Ala	Tyr	Leu	Val	Glu	Lys	Met	Arg	Gly	Gln	Phe	Gly	Trp	Val
			405						410					415	
Ser	Glu	Leu	His	Glu	Gly	Asn	Ile	Ser	Lys	Gln	Asp	Glu	Thr	Met	Met
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Thr	Asp	Leu	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Leu	Lys	Ile	Pro
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Leu	Glu	Glu	Ser	Ala	Glu	Ser	Ser	Asn	Phe	Ile	Gly	Tyr	Val	Val	Ala
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 Met Lys Leu Pro Leu Leu Met Phe Pro  
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gtg tgt ctg cta tgg ttg aaa gac tgt cat tgt gca cct act tgg aag 219  
 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
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gac aaa act gcc atc agt gaa aac gcg aac agt ttt tct gag gct ggg 267  
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cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
 Gln Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu  
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 Met Lys Thr Leu Lys Lys Cys Lys Glu Glu Lys Gln Glu Ala Leu Lys  
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ctt atg aat gaa gtt cat gaa cac ctg gag gag gaa gaa agc tta tgc 459  
 Leu Met Asn Glu Val His Glu His Leu Glu Glu Glu Glu Ser Leu Cys  
 90 95 100 105

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 Val Lys Asn Met Val Glu Gln Phe Phe Arg Lys Ile Tyr Gln Phe Leu  
 140 145 150

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 Phe Pro Leu Gln Glu Asn Asp Arg Ser Gly Pro Val Ser Lys Gly Val  
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 Thr Glu Glu Asp Ala Gln Val Ser His Ile Glu His Val Phe Ser Gln  
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ctg agc gca gat gtg aca tct ctc ttc aac aga agc ctt tac gtc ttc 747  
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 Lys Gln Leu Arg Arg Glu Phe Asp Gln Ala Phe Gln Ser Tyr Phe Thr  
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Ser Gly Thr Asp Val Thr Glu Pro Phe Phe Phe Pro Ser Leu Ser Lys	
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Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp Pro Pro Lys	
270 275 280	
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285 290 295	
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Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp	
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Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser	
315 320 325	
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Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu Asn Glu Ala	
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Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp Gln Val Val Gln	
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Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu Met Glu Lys Met	
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Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr Gln Ser Pro Gly	
380 385 390	
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Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val Ala Leu Ser Ala	
395 400 405	
cat gaa gga aat tct tct gat caa gat gac aca gtg gtt cct tca agc	1419
His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val Val Pro Ser Ser	
410 415 420 425	
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Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro Leu Glu Lys Ser	
430 435 440	
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Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu Lys Val Leu Gln	
445 450 455	

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 His Phe Lys Glu His Phe Lys Thr Trp  
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 35 40 45  
 Val Lys Ile Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu  
 50 55 60  
 Arg Arg Glu Glu Glu His Ser Lys Leu Met Lys Thr Leu Lys Lys Cys  
 65 70 75 80  
 Lys Glu Glu Lys Gln Glu Ala Leu Lys Leu Met Asn Glu Val His Glu  
 85 90 95  
 His Leu Glu Glu Glu Ser Leu Cys Gln Val Ser Leu Ala Asp Ser  
 100 105 110  
 Trp Asp Glu Cys Arg Ala Cys Leu Glu Ser Asn Cys Met Arg Phe Asp  
 115 120 125  
 Thr Thr Cys Gln Pro Ala Trp Ser Ser Val Lys Asn Met Val Glu Gln  
 130 135 140  
 Phe Phe Arg Lys Ile Tyr Gln Phe Leu Phe Pro Leu Gln Glu Asn Asp  
 145 150 155 160  
 Arg Ser Gly Pro Val Ser Lys Gly Val Thr Glu Glu Asp Ala Gln Val  
 165 170 175  
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 260 265 270  
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 275 280 285  
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 Gly Lys Leu Gly Gln Asn Leu Ser Asp Cys Val Asn Phe Arg Lys Arg  
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 Cys Gln Lys Cys Gln Asp Tyr Leu Ser Asp Asp Cys Pro Asn Val Pro  
 325 330 335  
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 Asn Gln Gln Tyr Asp Gln Val Val Gln Met Thr Gln Tyr His Leu Glu  
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Asp Thr Thr Leu Leu Met Glu Lys Met Arg Glu Gln Phe Gly Trp Val  
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 Ser Glu Leu Ala Tyr Gln Ser Pro Gly Ala Glu Asp Ile Phe Asn Pro  
 385 390 395 400  
 Val Lys Val Met Val Ala Leu Ser Ala His Glu Gly Asn Ser Ser Asp  
 405 410 415  
 Gln Asp Asp Thr Val Val Pro Ser Ser Leu Leu Pro Ser Ser Asn Phe  
 420 425 430  
 Thr Leu Ser Ser Pro Leu Glu Lys Ser Ala Gly Asn Ala Asn Phe Ile  
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 actgcaagga ttaacagtga gaac atg aag ctg cca ctt ttg atg ttt ccc 171  
 Met Lys Leu Pro Leu Leu Met Phe Pro  
 1 5  
  
 gtg tgt ctg cta tgg ttg aaa gac tgt cat tgt gca cct act tgg aag 219  
 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
 10 15 20 25  
  
 gac aaa act gcc atc agt gaa aac gcg aac agt ttt tct gag gct ggg 267  
 Asp Lys Thr Ala Ile Ser Glu Asn Ala Asn Ser Phe Ser Glu Ala Gly  
 30 35 40  
  
 gag ata gac gta gat gga gag gtg aag ata gct ttg att ggc att aaa 315  
 Glu Ile Asp Val Asp Gly Glu Val Lys Ile Ala Leu Ile Gly Ile Lys  
 45 50 55  
  
 cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
 Gln Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu  
 60 65 70  
  
 atg aaa acc ttg aag aag tgc aaa gaa gaa aag cag gag gcc ctg aaa 411  
 Met Lys Thr Leu Lys Lys Cys Lys Glu Glu Lys Gln Glu Ala Leu Lys  
 75 80 85  
  
 ctt atg aat gaa gtt cat gaa cac ctg gag gag gaa gaa agc tta tgc 459  
 Leu Met Asn Glu Val His Glu His Leu Glu Glu Glu Glu Ser Leu Cys  
 90 95 100 105  
  
 cag gtt tct ctg gca gat tcc tgg gat gaa tgc agg gct tgc ctg gaa 507  
 Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu Glu  
 110 115 120  
  
 agt aac tgc atg agg ttt gat acc acc tgc caa cct gca tgg tcc tct 555  
 Ser Asn Cys Met Arg Phe Asp Thr Thr Cys Gln Pro Ala Trp Ser Ser  
 125 130 135

gtg aaa aat atg gaa aat gac aga agt ggc cct gtc agc aaa ggg gtc	603
Val Lys Asn Met Glu Asn Asp Arg Ser Gly Pro Val Ser Lys Gly Val	
140 145 150	
act gag gaa gat gcg cag gtg tca cac ata gag cat gtg ttc agc cag	651
Thr Glu Glu Asp Ala Gln Val Ser His Ile Glu His Val Phe Ser Gln	
155 160 165	
ctg agc gca gat gtg aca tct ctc ttc aac aga agc ctt tac gtc ttc	699
Leu Ser Ala Asp Val Thr Ser Leu Phe Asn Arg Ser Leu Tyr Val Phe	
170 175 180 185	
aaa cag ctg cgg cga gaa ttt gac cag gct ttt cag tca tat ttc aca	747
Lys Gln Leu Arg Arg Glu Phe Asp Gln Ala Phe Gln Ser Tyr Phe Thr	
190 195 200	
tcg ggg act gac gtt aca gag cct ttc ttt ttt cca tct ttg tcc aag	795
Ser Gly Thr Asp Val Thr Glu Pro Phe Phe Phe Pro Ser Leu Ser Lys	
205 210 215	
gag cca gcc tac aga gca gat gct gag cca agc tgg gcc att ccc aat	843
Glu Pro Ala Tyr Arg Ala Asp Ala Glu Pro Ser Trp Ala Ile Pro Asn	
220 225 230	
gtc ttc cag ctg ctc tgc aac ttg agt ttc tca gtt tat caa agt gtc	891
Val Phe Gln Leu Leu Cys Asn Leu Ser Phe Ser Val Tyr Gln Ser Val	
235 240 245	
agt gaa aaa ctc atc aca acc ctg cgt gcc aca gag gac cct cca aaa	939
Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp Pro Pro Lys	
250 255 260 265	
caa gac aaa gac tcc aac cag gga ggc ccg att tca aag ata cta cct	987
Gln Asp Lys Asp Ser Asn Gln Gly Gly Pro Ile Ser Lys Ile Leu Pro	
270 275 280	
gag caa gac aga ggc tca gat ggg aaa ctt ggc cag aat ttg tct gat	1035
Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp	
285 290 295	
tgc gtt aat ttt cgc aag aga tgc cag aaa tgc cag gat tat cta tct	1083
Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser	
300 305 310	
gat gac tgc cct aat gtg cct gaa cta tac aga gaa ctc aat gag gcc	1131
Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu Asn Glu Ala	
315 320 325	
ctc cga ctg gtc agt aga tcc aat cag caa tac gac cag gtg gtg cag	1179
Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp Gln Val Val Gln	
330 335 340 345	
atg acc cag tat cac ctg gaa gac acc acg ctt ctg atg gag aag atg	1227
Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu Met Glu Lys Met	
350 355 360	
aga gag cag ttt ggc tgg gtt tct gaa ctg gca tac cag tcc cca gga	1275
Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr Gln Ser Pro Gly	
365 370 375	

gct gag gac atc ttt aat cca gtg aaa gta atg gta gcc cta agt gct	1323
Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val Ala Leu Ser Ala	
380 385 390	
cat gaa gga aat tct tct gat caa gat gac aca gtg gtt cct tca agc	1371
His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val Val Pro Ser Ser	
395 400 405	
ctc ctg cct tcc tct aac ttc aca ctc agc agc cct ctt gaa aag agt	1419
Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro Leu Glu Lys Ser	
410 415 420 425	
gct ggc aac gct aac ttc att gat cac gtg gta gag aag gtt ctt cag	1467
Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu Lys Val Leu Gln	
430 435 440	
cac ttt aag gag cac ttt aaa act tgg taagaagatt tagtccatcc	1514
His Phe Lys Glu His Phe Lys Thr Trp	
445 450	
tataatcagc aagaattaca ccttcggcca agacctgaga attctgaaaa tacaaagcag	1574
gctaacacaaa tgaacacagc tgcattgaaag ttaggtatat attaggaagc actattgggt	1634
tactttgttg aatggaagtt taatagctat tcaaattgag ttaatataaa aattttcttc	1694
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tactgagtcc cct	1767
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<212> PRT	
<213> Cavia sp.	
<400> 41	
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Asn Ala Asn Ser Phe Ser Glu Ala Gly Glu Ile Asp Val Asp Gly Glu	
35 40 45	
Val Lys Ile Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu	
50 55 60	
Arg Arg Glu Glu Glu His Ser Lys Leu Met Lys Thr Leu Lys Lys Cys	
65 70 75 80	
Lys Glu Glu Lys Gln Glu Ala Leu Lys Leu Met Asn Glu Val His Glu	
85 90 95	
His Leu Glu Glu Glu Ser Leu Cys Gln Val Ser Leu Ala Asp Ser	
100 105 110	
Trp Asp Glu Cys Arg Ala Cys Leu Glu Ser Asn Cys Met Arg Phe Asp	
115 120 125	
Thr Thr Cys Gln Pro Ala Trp Ser Ser Val Lys Asn Met Glu Asn Asp	
130 135 140	
Arg Ser Gly Pro Val Ser Lys Gly Val Thr Glu Glu Asp Ala Gln Val	
145 150 155 160	
Ser His Ile Glu His Val Phe Ser Gln Leu Ser Ala Asp Val Thr Ser	
165 170 175	
Leu Phe Asn Arg Ser Leu Tyr Val Phe Lys Gln Leu Arg Arg Glu Phe	
180 185 190	
Asp Gln Ala Phe Gln Ser Tyr Phe Thr Ser Gly Thr Asp Val Thr Glu	
195 200 205	
Pro Phe Phe Phe Pro Ser Leu Ser Lys Glu Pro Ala Tyr Arg Ala Asp	

210	Ala Glu Pro Ser Trp	215	Ala Ile Pro Asn Val	220	Phe Gln Leu Leu Cys Asn
225	Leu Ser Phe Ser Val	230	Tyr Gln Ser Val	235	Glu Lys Leu Ile Thr Thr
	245		250		255
Leu Arg Ala Thr	Glu Asp Pro Pro	Lys Gln Asp Lys	Asp Ser Asn Gln		
	260		265		270
Gly Gly Pro Ile	Ser Lys Ile Leu	Pro Glu Gln Asp	Arg Gly Ser Asp		
	275		280		285
Gly Lys Leu Gly	Gln Asn Leu Ser	Asp Cys Val Asn	Phe Arg Lys Arg		
	290		295		300
Cys Gln Lys Cys	Gln Asp Tyr Leu	Ser Asp Asp Cys	Pro Asn Val Pro		
	305		310		315
Glu Leu Tyr Arg	Glu Leu Asn Glu	Ala Leu Arg Leu	Val Ser Arg Ser		
	325		330		335
Asn Gln Gln Tyr	Asp Gln Val Val	Gln Met Thr Gln	Tyr His Leu Glu		
	340		345		350
Asp Thr Thr Leu	Leu Met Glu Lys	Met Arg Glu Gln	Phe Gly Trp Val		
	355		360		365
Ser Glu Leu Ala	Tyr Gln Ser Pro	Gly Ala Glu Asp	Ile Phe Asn Pro		
	370		375		380
Val Lys Val Met	Val Ala Leu Ser	Ala His Glu Gly	Asn Ser Ser Asp		
	385		390		395
Gln Asp Asp Thr	Val Val Pro Ser	Ser Leu Leu Pro	Ser Ser Asn Phe		
	405		410		415
Thr Leu Ser Ser	Pro Leu Glu Lys	Ser Ala Gly Asn	Ala Asn Phe Ile		
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Asp His Val Val	Glu Lys Val Leu	Gln His Phe Lys	Glu His Phe Lys		
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Thr Trp					
450					

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 <213> Cavia sp.

<220>  
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 aatcatgatac aaggagctac acactctgac ttaactttat tctgtggaca atgagagaca 120  
 actgcaagga ttaacagtga gaac atg aag ctg cca ctt ttg atg ttt ccc 171  
 Met Lys Leu Pro Leu Leu Met Phe Pro  
 1 5

gtg tgt ctg cta tgg ttg aaa gac tgt cat tgt gca cct act tgg aag 219  
 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
 10 15 20 25

gac aaa act gcc atc agt gaa aac gcg aac agt ttt tct gag gct ggg 267  
 Asp Lys Thr Ala Ile Ser Glu Asn Ala Asn Ser Phe Ser Glu Ala Gly  
 30 35 40

gag ata gac gta gat gga gag gtg aag ata gct ttg att ggc att aaa 315  
 Glu Ile Asp Val Asp Gly Glu Val Lys Ile Ala Leu Ile Gly Ile Lys  
 45 50 55

cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
 Gln Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu

60	65	70	
atg aaa acc ttg aag aag tgc aaa gaa gaa aag cag gag gcc ctg aaa Met Lys Thr Leu Lys Lys Cys Lys Glu Glu Lys Gln Glu Ala Leu Lys 75 80 85			411
ctt atg aat gaa gtt cat gaa cac ctg gag gag gaa gaa agc tta tgc Leu Met Asn Glu Val His Glu His Leu Glu Glu Glu Glu Ser Leu Cys 90 95 100 105			459
cag gtt tct ctg gca gat tcc tgg gat gaa tgc agg gct tgc ctg gaa Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu Glu 110 115 120			507
agt aac tgc atg agg ttt gat acc acc tgc caa cct gca tgg tcc tct Ser Asn Cys Met Arg Phe Asp Thr Thr Cys Gln Pro Ala Trp Ser Ser 125 130 135			555
gtg aaa aat atg gag cca gcc tac aga gca gat gct gag cca agc tgg Val Lys Asn Met Glu Pro Ala Tyr Arg Ala Asp Ala Glu Pro Ser Trp 140 145 150			603
gcc att ccc aat gtc ttc cag ctg ctc tgc aac ttg agt ttc tca gtt Ala Ile Pro Asn Val Phe Gln Leu Leu Cys Asn Leu Ser Phe Ser Val 155 160 165			651
tat caa agt gtc agt gaa aaa ctc atc aca acc ctg cgt gcc aca gag Tyr Gln Ser Val Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu 170 175 180 185			699
gac cct cca aaa caa gac aaa gac tcc aac cag gga ggc ccg att tca Asp Pro Pro Lys Gln Asp Lys Asp Ser Asn Gln Gly Gly Pro Ile Ser 190 195 200			747
aag ata cta cct gag caa gac aga ggc tca gat ggg aaa ctt ggc cag Lys Ile Leu Pro Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln 205 210 215			795
aat ttg tct gat tgc gtt aat ttt cgc aag aga tgc cag aaa tgc cag Asn Leu Ser Asp Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln 220 225 230			843
gat tat cta tct gat gac tgc cct aat gtg cct gaa cta tac aga gaa Asp Tyr Leu Ser Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu 235 240 245			891
ctc aat gag gcc ctc cga ctg gtc agt aga tcc aat cag caa tac gac Leu Asn Glu Ala Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp 250 255 260 265			939
cag gtg gtg cag atg acc cag tat cac ctg gaa gac acc acg ctt ctg Gln Val Val Gln Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu 270 275 280			987
atg gag aag atg aga gag cag ttt ggc tgg gtt tct gaa ctg gca tac Met Glu Lys Met Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr 285 290 295			1035
cag tcc cca gga gct gag gac atc ttt aat cca gtg aaa gta atg gta Gln Ser Pro Gly Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val 300 305 310			1083

gcc cta agt gct cat gaa gga aat tct tct gat caa gat gac aca gtg 1131  
Ala Leu Ser Ala His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val  
315 320 325

gtt cct tca agc ctc ctg cct tcc tct aac ttc aca ctc agc agc cct 1179  
Val Pro Ser Ser Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro  
330 335 340 345

ctt gaa aag agt gct ggc aac gct aac ttc att gat cac gtg gta gag 1227  
Leu Glu Lys Ser Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu  
350 355 360

aag gtt ctt cag cac ttt aag gag cac ttt aaa act tgg taagaagatt 1276  
Lys Val Leu Gln His Phe Lys Glu His Phe Lys Thr Trp  
365 370

tagtccatcc tataatcagc aagaattaca ccttcggcca agacctgaga attctgaaaa 1336  
tacaagcag gctaacacaa tgaacacagc tgcataaag ttaggtatat attaggaagc 1396  
actattgggtt tactttgttg aatggaagtt taatagctat tcaaattgag ttaatatataa 1456  
aatttcttcc taaaaagtaa aatgtacata tgtagaatat gatgcattag ttctttgtat 1516  
actaaataaa tactgagtc cct 1539

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<211> 374  
<212> PRT  
<213> Cavia sp.

<400> 43  
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20 25 30  
Asn Ala Asn Ser Phe Ser Glu Ala Gly Glu Ile Asp Val Asp Gly Glu  
35 40 45  
Val Lys Ile Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu  
50 55 60  
Arg Arg Glu Glu Glu His Ser Lys Leu Met Lys Thr Leu Lys Lys Cys  
65 70 75 80  
Lys Glu Glu Lys Gln Glu Ala Leu Lys Leu Met Asn Glu Val His Glu  
85 90 95  
His Leu Glu Glu Glu Glu Ser Leu Cys Gln Val Ser Leu Ala Asp Ser  
100 105 110  
Trp Asp Glu Cys Arg Ala Cys Leu Glu Ser Asn Cys Met Arg Phe Asp  
115 120 125  
Thr Thr Cys Gln Pro Ala Trp Ser Ser Val Lys Asn Met Glu Pro Ala  
130 135 140  
Tyr Arg Ala Asp Ala Glu Pro Ser Trp Ala Ile Pro Asn Val Phe Gln  
145 150 155 160  
Leu Leu Cys Asn Leu Ser Phe Ser Val Tyr Gln Ser Val Ser Glu Lys  
165 170 175  
Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp Pro Pro Lys Gln Asp Lys  
180 185 190  
Asp Ser Asn Gln Gly Gly Pro Ile Ser Lys Ile Leu Pro Glu Gln Asp  
195 200 205  
Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp Cys Val Asn  
210 215 220  
Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser Asp Asp Cys  
225 230 235 240  
Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu Asn Glu Ala Leu Arg Leu

				245					250					255			
Val	Ser	Arg	Ser	Asn	Gln	Gln	Tyr	Asp	Gln	Val	Val	Gln	Met	Thr	Gln		
			260					265					270				
Tyr	His	Leu	Glu	Asp	Thr	Thr	Leu	Leu	Met	Glu	Lys	Met	Arg	Glu	Gln		
		275					280					285					
Phe	Gly	Trp	Val	Ser	Glu	Leu	Ala	Tyr	Gln	Ser	Pro	Gly	Ala	Glu	Asp		
	290					295					300						
Ile	Phe	Asn	Pro	Val	Lys	Val	Met	Val	Ala	Leu	Ser	Ala	His	Glu	Gly		
305					310					315					320		
Asn	Ser	Ser	Asp	Gln	Asp	Asp	Thr	Val	Val	Pro	Ser	Ser	Leu	Leu	Pro		
			325						330					335			
Ser	Ser	Asn	Phe	Thr	Leu	Ser	Ser	Pro	Leu	Glu	Lys	Ser	Ala	Gly	Asn		
		340						345				350					
Ala	Asn	Phe	Ile	Asp	His	Val	Val	Glu	Lys	Val	Leu	Gln	His	Phe	Lys		
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Glu	His	Phe	Lys	Thr	Trp												
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 <212> DNA  
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<220>  
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 actgcaagga ttaacagtga gaac atg aag ctg cca ctt ttg atg ttt ccc 171  
 Met Lys Leu Pro Leu Leu Met Phe Pro  
 1 5

gtg tgt ctg cta tgg ttg aaa gac tgt cat tgt gca cct act tgg aag 219  
 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
 10 15 20 25

gac aaa act gcc atc agt gaa aac gcg aac agt ttt tct gag gct ggg 267  
 Asp Lys Thr Ala Ile Ser Glu Asn Ala Asn Ser Phe Ser Glu Ala Gly  
 30 35 40

gag ata gac gta gat gga gag gtg aag ata gct ttg att ggc att aaa 315  
 Glu Ile Asp Val Asp Gly Glu Val Lys Ile Ala Leu Ile Gly Ile Lys  
 45 50 55

cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
 Gln Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu  
 60 65 70

atg aaa acc ttg aag aag tgc aaa gaa gaa aag cag gag gcc ctg aaa 411  
 Met Lys Thr Leu Lys Lys Cys Lys Glu Glu Lys Gln Glu Ala Leu Lys  
 75 80 85

ctt atg aat gaa gtt cat gaa cac ctg gag gag gaa gaa agc tta tgc 459  
 Leu Met Asn Glu Val His Glu His Leu Glu Glu Glu Glu Ser Leu Cys  
 90 95 100 105

cag gtt tct ctg gca gat tcc tgg gat gaa tgc agg gct tgc ctg gaa 507  
 Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu Glu  
 110 115 120

agt aac tgc atg agg ttt gat acc acc tgc caa cct gca tgg tcc tct	555
Ser Asn Cys Met Arg Phe Asp Thr Thr Cys Gln Pro Ala Trp Ser Ser	
125 130 135	
gtg aaa aat atg cca gcc tac aga gca gat gct gag cca agc tgg gcc	603
Val Lys Asn Met Pro Ala Tyr Arg Ala Asp Ala Glu Pro Ser Trp Ala	
140 145 150	
att ccc aat gtc ttc cag ctg ctc tgc aac ttg agt ttc tca gtt tat	651
Ile Pro Asn Val Phe Gln Leu Leu Cys Asn Leu Ser Phe Ser Val Tyr	
155 160 165	
caa agt gtc agt gaa aaa ctc atc aca acc ctg cgt gcc aca gag gac	699
Gln Ser Val Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp	
170 175 180 185	
cct cca aaa caa gac aaa gac tcc aac cag gga ggc ccg att tca aag	747
Pro Pro Lys Gln Asp Lys Asp Ser Asn Gln Gly Gly Pro Ile Ser Lys	
190 195 200	
ata cta cct gag caa gac aga ggc tca gat ggg aaa ctt ggc cag aat	795
Ile Leu Pro Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn	
205 210 215	
ttg tct gat tgc gtt aat ttt cgc aag aga tgc cag aaa tgc cag gat	843
Leu Ser Asp Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp	
220 225 230	
tat cta tct gat gac tgc cct aat gtg cct gaa cta tac aga gaa ctc	891
Tyr Leu Ser Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu	
235 240 245	
aat gag gcc ctc cga ctg gtc agt aga tcc aat cag caa tac gac cag	939
Asn Glu Ala Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp Gln	
250 255 260 265	
gtg gtg cag atg acc cag tat cac ctg gaa gac acc acg ctt ctg atg	987
Val Val Gln Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu Met	
270 275 280	
gag aag atg aga gag cag ttt ggc tgg gtt tct gaa ctg gca tac cag	1035
Glu Lys Met Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr Gln	
285 290 295	
tcc cca gga gct gag gac atc ttt aat cca gtg aaa gta atg gta gcc	1083
Ser Pro Gly Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val Ala	
300 305 310	
cta agt gct cat gaa gga aat tct tct gat caa gat gac aca gtg gtt	1131
Leu Ser Ala His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val Val	
315 320 325	
cct tca agc ctc ctg cct tcc tct aac ttc aca ctc agc agc cct ctt	1179
Pro Ser Ser Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro Leu	
330 335 340 345	
gaa aag agt gct ggc aac gct aac ttc att gat cac gtg gta gag aag	1227
Glu Lys Ser Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu Lys	
350 355 360	
gtt ctt cag cac ttt aag gag cac ttt aaa act tgg taagaagatt	1273
Val Leu Gln His Phe Lys Glu His Phe Lys Thr Trp	

tagtccatcc	tataatcagc	aagaattaca	ccttcggcca	agacctgaga	attctgaaaa	1333
tacaaagcag	gctaacacaa	tgaacacagc	tgcatgaaag	ttaggtatat	attaggaagc	1393
actattgggtt	tactttgttg	aatggaagtt	taatagctat	tcaaattgag	ttaatatataa	1453
aattttcttcc	taaaaagtaa	aatgtacata	tgtagaatat	gatgcattag	ttctttgtat	1513
actaaataaaa	tactgagtcc	cct				1536

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 <211> 373  
 <212> PRT  
 <213> *Cavia* sp.

<400> 45

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			20					25					30		
Asn	Ala	Asn	Ser	Phe	Ser	Glu	Ala	Gly	Glu	Ile	Asp	Val	Asp	Gly	Glu
			35				40					45			
Val	Lys	Ile	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
	50					55					60				
Arg	Arg	Glu	Glu	Glu	His	Ser	Lys	Leu	Met	Lys	Thr	Leu	Lys	Lys	Cys
65					70					75					80
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Leu	Lys	Leu	Met	Asn	Glu	Val	His	Glu
				85					90					95	
His	Leu	Glu	Glu	Glu	Glu	Ser	Leu	Cys	Gln	Val	Ser	Leu	Ala	Asp	Ser
				100				105						110	
Trp	Asp	Glu	Cys	Arg	Ala	Cys	Leu	Glu	Ser	Asn	Cys	Met	Arg	Phe	Asp
			115				120					125			
Thr	Thr	Cys	Gln	Pro	Ala	Trp	Ser	Ser	Val	Lys	Asn	Met	Pro	Ala	Tyr
	130					135						140			
Arg	Ala	Asp	Ala	Glu	Pro	Ser	Trp	Ala	Ile	Pro	Asn	Val	Phe	Gln	Leu
145					150					155					160
Leu	Cys	Asn	Leu	Ser	Phe	Ser	Val	Tyr	Gln	Ser	Val	Ser	Glu	Lys	Leu
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His	Leu	Glu	Asp	Thr	Thr	Leu	Leu	Met	Glu	Lys	Met	Arg	Glu	Gln	Phe
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Gly	Trp	Val	Ser	Glu	Leu	Ala	Tyr	Gln	Ser	Pro	Gly	Ala	Glu	Asp	Ile
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Phe	Asn	Pro	Val	Lys	Val	Met	Val	Ala	Leu	Ser	Ala	His	Glu	Gly	Asn
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Ser	Ser	Asp	Gln	Asp	Asp	Thr	Val	Val	Pro	Ser	Ser	Leu	Leu	Pro	Ser
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	Met Lys Pro Pro Ile Leu Val Phe Ile Val Tyr Leu Leu
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Gln Leu Arg Asp Cys Gln Cys Ala Pro Thr Gly Lys Asp Arg Thr Ser	
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Ile Arg Glu Asp Pro Lys Gly Phe Ser Lys Ala Gly Glu Ile Asp Val	
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Asp Glu Glu Val Lys Lys Ala Leu Ile Gly Met Lys Gln Met Lys Ile	
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Leu Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu Met Arg Thr Leu	
65 70 75	
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Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala Leu Lys Leu Met Asn Glu	
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Val Gln Glu His Leu Glu Glu Glu Glu Arg Leu Cys Gln Val Ser Leu	
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Met Gly Ser Trp Asp Glu Cys Lys Ser Cys Leu Glu Ser Asp Cys Met	
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Arg Phe Tyr Thr Thr Cys Gln Ser Ser Trp Ser Ser Met Lys Ser Thr	
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Ile Glu Arg Val Phe Arg Lys Ile Tyr Gln Phe Leu Phe Pro Phe His	
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Asp Val Gln Leu Met Gln Ile Glu Asn Val Phe Ser Gln Leu Thr Val	
175 180 185	
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Asp Val Gly Phe Leu Tyr Asn Met Ser Phe His Val Phe Lys Gln Met	
190 195 200 205	
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Gln Gln Glu Phe Asp Leu Ala Phe Gln Ser Tyr Phe Met Ser Asp Thr	
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Asp Ser Met Glu Pro Tyr Phe Phe Pro Ala Phe Ser Lys Glu Pro Ala	
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Lys Lys Ala His Pro Met Gln Ser Trp Asp Ile Pro Ser Phe Phe Gln	
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<400> 49

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Asp	Pro	Lys	Gly	Phe	Ser	Lys	Ala	Gly	Glu	Ile	Asp	Val	Asp	Glu	Glu
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His	Leu	Glu	Glu	Glu	Glu	Arg	Leu	Cys	Gln	Val	Ser	Leu	Met	Gly	Ser
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Trp	Asp	Glu	Cys	Lys	Ser	Cys	Leu	Glu	Ser	Asp	Cys	Met	Arg	Phe	Tyr
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Cys	Gly	Glu	Pro	Gly	Gln	Asn	Ser	Ser	Glu	Cys	Leu	Gln	Phe	His	Ala
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	260	265
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	275	280
Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys		285
	290	295
Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His		300
305	310	315
Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln		320
	325	330
Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala		335
	340	345
Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu		350
	355	360
Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val		365
	370	375
Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met		380
385	390	395
Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile		400
	405	410
Pro Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val		415
	420	425
Ala Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp		430
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44

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<400> 54

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<210> 56  
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<400> 57  
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36

<210> 61

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<220>

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<210> 64

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<212> PRT

<213> Homo sapiens

<400> 64

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Asp	Ser	His	Cys	Ala	Pro	Thr	Trp	Lys	Asp	Lys	Thr	Ala	Ile	Ser	Glu
			20					25					30		
Asn	Leu	Lys	Ser	Phe	Ser	Glu	Val	Gly	Glu	Ile	Asp	Ala	Asp	Glu	Glu
			35				40					45			
Val	Lys	Lys	Ala	Leu	Thr	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
			50			55				60					
Arg	Lys	Glu	Lys	Glu	His	Thr	Asn	Leu	Met	Ser	Thr	Leu	Lys	Lys	Cys
65					70				75					80	
Arg	Glu	Glu	Lys	Gln	Glu	Ala	Leu	Lys	Leu	Leu	Asn	Glu	Val	Gln	Glu
				85				90						95	
His	Leu	Glu	Glu	Glu	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser
			100				105						110		
Trp	Gly	Glu	Cys	Arg	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr



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atgaggacct gggactacag gacacagcta aatccctgac acggatgaaa attaaagcag 300
agaaaaacga aggtccttcc agaagctggt ggcaacttca ctggggagat attgcaaata 360
acagcgggaa catgaagccg ccactcttgg tgtttattgt gtgtctgctg tggttgaaag 420
acagtcactg cgcacccact tgggaaggaca aaactgctat cagtgaaaac ctgaagagtt 480
tttctgaggt gggggagata gatgcagatg aagagggtgaa gaaggctttg actggtatta 540
agcaaatagaa aatcatgatg gaaagaaaag agaaggaaca caccaatcta atgagcacc 600
tgaagaaatg cagagaagaa aagcaggagg ccctgaaact tctgaatgaa gttcaagaac 660
atctggagga agaagaaagg ctatgccggg agtctttggc agattcctgg ggtgaatgca 720
ggtcttgctt ggaaaataac tgcattgagaa ttatatacaac ctgccaacct agctggctct 780
ctgtgaaaaa taagctcctg accacggagg cctgatttca aagatgttac ntgggcagga 840
cagaggactg tgtggggaac ttgaccagaa tttgtcaaga tgtttcaaat ttcattgaaa 900
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 <213> Homo sapiens

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20          25          30
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35          40          45
Pro Ser Leu Leu Pro Gly Trp Ser Ser Val Ala Cys Ser Leu Thr Glu
50          55          60
Ala Ser Asn Ser Trp Val Gln Val Thr Leu Pro Pro Gln Pro His Glu
65          70          75          80
Asp Leu Gly Leu Gln Asp Thr Ala Lys Ser Leu Thr Arg Met Lys Ile
85          90          95
Lys Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His
100         105         110
Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu
115         120         125
Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro
130         135         140
Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser
145         150         155         160
Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr
165         170         175
Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His
180         185         190
Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu
195         200         205
Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu
210         215         220
Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser
225         230         235         240
Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser
245         250         255

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Trp	Ser	Ser	Val	Lys	Asn	Lys	Leu	Leu	Thr	Thr	Glu	Ala	Phe	Gln	Arg	
			260					265					270			
Cys	Tyr	Leu	Gly	Arg	Thr	Glu	Asp	Cys	Val	Gly	Asn	Leu	Thr	Arg	Ile	
		275					280					285				
Cys	Gln	Asp	Val	Ser	Asn	Phe	Met	Lys	Asn	Ala	Lys	Asn	Val	Arg	Leu	
	290					295					300					
Thr	Tyr	Leu	Lys	Thr	Val	Leu	Met	Tyr	Leu	Leu	Cys	Thr	Gln	Asn	Thr	
305					310					315					320	
Arg	Arg	Ser	Gly	Trp	Ser	Met	Tyr	Pro	Ile	Ser	Ser	Met	Ala	Arg	Phe	
			325						330					335		
Ser	Arg	Pro	Gly	Ser	Thr	Trp	Arg	Thr	Pro	Pro	Ile	Trp	Trp	Arg	Arg	
			340					345					350			
Glu	Gly	Asn	Leu	Ala	Gly	Cys	Leu	Asn	Trp	Gln	Thr	Arg	Pro	Gln	Lys	
		355					360					365				
Gln	Arg	Ser	Ser	Leu	Ile	Gln	Tyr	Arg	Phe	Gln	Gly	Phe	Met	Lys	Glu	
	370					375					380					
Ile	Phe	Pro	Asn	Lys	Met	Lys	Gln	Gln	Thr	Ala	Phe	Cys	Leu	Pro	Leu	
385					390					395					400	
Ile	Ser	His	Ser	Arg	Ser	Leu	Leu	Lys	Lys	Val	Leu	Arg	Val	Leu	Thr	
			405						410					415		
Ser	Leu	Ala	Thr	Trp	Gln	Lys	Leu	Tyr	Ser	Ile	Leu	Arg	Asn	Ile	Leu	
			420					425					430			
Lys	Pro	Gly	Lys	Lys	Ile	Cys	Ile	Leu	Tyr	Pro	Val	Ser	Arg	Ile	Ile	
		435					440						445			
Ser	Ser	Ser	Gly	Thr	Trp	Lys	Ser	Asn	Lys	Lys	Gly	Cys	Asn	Lys	His	
	450					455					460					
Ser	Cys	Arg	Lys	Val	Cys	Leu	Tyr	Thr	Met	Lys	Tyr	Ser	Phe	Thr	Tyr	
465					470					475					480	
Val	Glu	Trp	Leu	Ser	Tyr	Tyr	Ser	Asn	Val	Lys	Met	Lys	Ile	Pro	Pro	
			485						490					495		
Lys	Ile	Lys	Arg	Asn	Met	Tyr	Tyr	Ile	Ser	Trp	Tyr	Ile	Ser	Ser	Ser	
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<220>  
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<400> 67  
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<210> 68  
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<400> 69  
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<210> 71  
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<400> 71  
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<210> 72  
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<400> 72  
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 attcattgct ttgttttgta aagaccaata ggttctgtat agtctttttt taaattgtgg 180  
 taaaatacac atggcattaa ttaccatttt taaccatttt aaagtgcaca atttgtggca 240  
 ttaagtacac tcacgttgct gtgcaaccat caccaccgtc catcttcaga acctttttat 300  
 cttcctaaac tgaaactctg tactcgtaa gcactcactt cccttttccc catccccag 360  
 cccgtagcaa ccacgactgt actttctatg aatttgacta ctctaggtac tgcattgtagg 420  
 tggaatcata cagtatttgg cttttgcttg ntttgntttg ttttttgttt tctaagacag 480  
 ggtctcactc tgtcgcccta gctggattgc agagttaagt ttatgattat gaaataaaaa 540  
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<210> 74

<211> 1161  
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<400> 74  
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 ggtttaagag gaaagctggt tcgtggggat tggatgggag gccaccagga aaccaagttc 180  
 ccgcgccagc ttcagtgtct tcctcttTcc gccgcctttg ccccgcccac atcactttcg 240  
 ctccagtttt tgaaaacgct gcgaagcgga atgggtccaca ggggaaaacg gaggaggggc 300  
 caaagccagg actttgagac cggcgcgcgg tcaagcccag gcagctctcc ctaaccctcc 360  
 agcactgggc aaacgctgcc cgatgacgcc cgctcgggg gccacggcat cactggggcg 420  
 actgcgagcc cggcccgga gccgctggga cggcgcttac ctcccggctg tcgtgtgtgt 480  
 gtgtgtttgc cgcgccagtc acgtccctaa tgggaccctc cgtttcggcg tctgtaaggc 540  
 gaggaggacg atgcgtcccc tccctsgcag gattgaggtt aggactaaac ggggtccgca 600  
 gcgcccggca gctcccgagc gctctcccca gccgcgcctc cctccttccc gccaccgctc 660  
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 aggggtgccg tgcccgtgcg gtcgtccttc ctgacgcgcg agcggaggat gtgttgatc 780  
 tgccccagga tttccaggtc ccagatgaag agataattct acttactgga tataggatgc 840  
 attagatctt cttaccttaa aaaaaaaaaa aaaggcagca atgatcaaaa tactaataaa 900  
 ttactcacag actcagtgt ttttttcttg gagtaaaagt ccaggatggg taatagaata 960  
 cctgtctgtt gcttttgga aaattggtac tgtatgtagc aaaataatgt gaaaccata 1020  
 tgcattgata ttcttaacaa tttgaagaaa tcgtcacagc tttcctgggt tggtgagcct 1080  
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 20 25 30  
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 35 40 45  
 Gly Val Cys Lys Ala Arg Arg Thr Met Arg Pro Leu Pro Xaa Arg Ile  
 50 55 60  
 Glu Val Arg Thr Lys Arg Gly Pro Gln Arg Pro Ala Ala Pro Glu Arg  
 65 70 75 80  
 Ser Pro Gln Pro Arg Leu Pro Pro Ser Arg His Pro Ser Arg Arg Gly  
 85 90 95  
 Pro Arg Arg His Leu Ser Gly Cys Ser Ala Pro Ala Cys Arg Ile Pro  
 100 105 110  
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<210> 76  
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 <212> PRT  
 <213> Homo sapiens

<400> 76  
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 Leu Pro Ser Ala Leu Pro Ser Arg Ala Ser Leu Leu Pro Ala Trp Ala  
           35                          40                          45  
 Gly Arg Val Thr Ser Gln Ala Val Ala Arg Leu His Ala Glu Tyr Arg  
           50                          55                          60  
 Gln Gly Ala Gly Ala Arg Ala Val Val Leu Pro Asp Ala Ala Ala Glu  
   65                          70                          75                          80  
 Asp Val Leu Asp Leu Pro Gln Asp Phe Gln Val Pro Asp Glu Glu Ile  
                           85                          90                          95  
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<223> Primer

<400> 107  
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<220>

<223> Primer

<400> 108  
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<210> 109  
<211> 117  
<212> DNA  
<213> Rattus

<400> 109  
gtctcaactg gcaagccata accagtgact gaggacatct ttaattcaac aaaggcagtt 60  
ccaaagattc atggaggaga ttcttccaag caggatgaaa ttatggtaga ctcaagc 117

<210> 110  
 <211> 39  
 <212> PRT  
 <213> Rattus

<400> 110  
 Ser Gln Leu Ala Ser His Asn Pro Val Thr Glu Asp Ile Phe Asn Ser  
 1 5 10 15  
 Thr Lys Ala Val Pro Lys Ile His Gly Gly Asp Ser Ser Lys Gln Asp  
 20 25 30  
 Glu Ile Met Val Asp Ser Ser  
 35

<210> 111  
 <211> 289  
 <212> DNA  
 <213> Rattus

<400> 111  
 cataacccag tgactgagga catctttaat tcaacaaagg cagttccaaa gattcatgga 60  
 ggagattctt ccaagcagga tgaaattatg gtagactcaa gcagcattct gccttcctct 120  
 aacttcaccg tccagaatcc tcctgaagaa ggtgctgaga gctcaaagt tatttactac 180  
 atggcagcta aagttctgca gcatctaaag ggatgttttg aaacttggtg agaatagctg 240  
 attaggaaag ctttggtgag agggtaggta acataaaaaa aaaaaaaaaa 289

<210> 112  
 <211> 92  
 <212> PRT  
 <213> Rattus

<400> 112  
 His Asn Pro Val Thr Glu Asp Ile Phe Asn Ser Thr Lys Ala Val Pro  
 1 5 10 15  
 Lys Ile His Gly Gly Asp Ser Ser Lys Gln Asp Glu Ile Met Val Asp  
 20 25 30  
 Ser Ser Ser Ile Leu Pro Ser Ser Asn Phe Thr Val Gln Asn Pro Pro  
 35 40 45  
 Glu Glu Gly Ala Glu Ser Ser Asn Val Ile Tyr Tyr Met Ala Ala Lys  
 50 55 60  
 Val Leu Gln His Leu Lys Gly Cys Phe Glu Thr Trp Glu Leu Ile Arg  
 65 70 75 80  
 Lys Ala Leu Leu Arg Gly Val Thr Lys Lys Lys Lys  
 85 90

<210> 113  
 <211> 1120  
 <212> DNA  
 <213> Rattus

<400> 113  
 cccttcactg cgcgccact gggaaggaga cagatgctac ggatggaaac ctaaagagtc 60  
 ttccagaggt aggagaggca gatgtagagg gagaggtaa gaaggctttg attggcatta 120  
 agcaaatgaa aatcatgatg gaaaggagag aggaggaaca cgcaaaattg atgaaagcct 180  
 tgaagaagtg caaagaagaa aagcaggagg cccagaaact catgaacgaa gtgcaagaac 240  
 gtctggagga agaagaaaag ctatgtcagg catcttctat aggttcttgg gatggatgca 300  
 ggccatgttt ggaaagtaac tgcatacgat tttatacagc ttgccaacct ggttggtcct 360  
 ctgtgaaaag catgatgaag caatttctca agaagatata ccgatttctg tcttcccaga 420  
 gtgaagatgt aaaggatccc cctgccatag aacagctgac taaggaagat ttacaagtgg 480  
 tacacataga gaacctgttt agccagctgg ccgtggatgc aaaatctctc ttcaacatga 540  
 gctttttacat ttttaagcag atgcagcaag aatttgatca ggcttttcaa ttatacttca 600  
 tgtccgatgt ggacttaatg gagccatacc cccagctttt atctaaagag ataatcaaaa 660  
 aagaagaact tgggcaaagg tggggcattc ccaatgtctt ccagctgttt cataatttca 720

gtctctctgt	ttatgggaga	gtccaacaaa	taataatgaa	gacactcaat	gcaattgaag	780
attcatggga	accacacaaa	gagttagacc	agagaggtat	gacttcagag	atgttacctg	840
agcaaaatgg	agaaatgtgt	gaggaatttg	tcaagaattt	atctggatgt	ttaaaatttc	900
gtaaaagatg	caaaaaatgt	cacaattacc	tatctgaaga	atgccctgat	gtacctgaac	960
ttcacataga	attccttgag	gccctgaaat	tagtcaatgt	atccaatcag	caatatgatc	1020
agattgtcca	gatgaccag	tatcatttgg	aagataccat	atacctgatg	gagaaaatgc	1080
aagagcagtt	tggatgggtg	tctcaactgg	caagccataa			1120

<210> 114

<211> 397

<212> PRT

<213> Rattus

<400> 114

Leu	His	Cys	Ala	Pro	Thr	Gly	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly	Asn	
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Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu	Val	
			20					25					30			
Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	
		35					40					45				
Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys	Lys	
	50					55					60					
Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu	Arg	
65					70					75					80	
Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser	Trp	
				85					90					95		
Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr	Thr	
			100					105					110			
Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	Phe	
		115					120					125				
Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	Lys	
	130					135					140					
Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	Val	
145					150					155					160	
His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	Leu	
			165						170					175		
Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	Asp	
		180						185					190			
Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	Pro	
	195						200					205				
Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu	Gly	
	210					215					220					
Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	Ser	
225					230					235					240	
Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	Asn	
			245						250					255		
Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	Gly	
		260						265					270			
Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	Glu	
		275					280					285				
Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	Gln	
	290					295					300					
Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	Leu	
305					310					315					320	
His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	Gln	
			325						330					335		
Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	Thr	
		340						345					350			
Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	Gln	
	355					360					365					
Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys	
	370					375					380					

Ala Val Pro Lys Ile His Gly Gly Asp Ser Ser Lys Gln  
 385 390 395

<210> 115  
 <211> 341  
 <212> DNA  
 <213> Rattus

<400> 115  
 tttttttttt tttttttcaa ggcttttcac aattttgcgt gttcctctct tctcctttcc 60  
 atcatgattt tcatttgctt aatgccaatc aaagccttct tgacctctcc ctctacatct 120  
 gcctctccta cctctggaag actcttttagg tttccatccg tagcatctgt ctctttccaa 180  
 gtaggtgcac tgtcacaata tttcaacct aacagatata cagaaatcac aaagagtggg 240  
 ggctgcatgg tccagtgttc caccgatatt gcagctctcc ccagagaaat tgccactaac 300  
 ttctgaaagg accttcactt tttacgatgt gcctcgtgcc g 341

<210> 116  
 <211> 341  
 <212> DNA  
 <213> Rattus

<400> 116  
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 gggagagctg caatatcggt ggaacactgg accatgcagc caccactctt tgtgatttct 120  
 gtgtatctgt tatggttgaa atattgtgac agtgcaccta cttggaagga gacagatgct 180  
 acggatggaa acctaaagag tcttccagag gtaggagagg cagatgtaga gggagaggtc 240  
 aagaaggctt tgattggcat taagcaaata aaaatcatga tggaaaggag agaggaggaa 300  
 caccgaaaat tgatgaaagc cttgaaaaaa aaaaaaaaaa a 341

<210> 117  
 <211> 112  
 <212> PRT  
 <213> Rattus

<400> 117  
 Arg His Glu Ala His Arg Lys Lys Arg Ser Phe Gln Lys Leu Val Ala  
 1 5 10 15  
 Ile Ser Leu Gly Arg Ala Ala Ile Ser Val Glu His Trp Thr Met Gln  
 20 25 30  
 Pro Pro Leu Phe Val Ile Ser Val Tyr Leu Leu Trp Leu Lys Tyr Cys  
 35 40 45  
 Asp Ser Ala Pro Thr Trp Lys Glu Thr Asp Ala Thr Asp Gly Asn Leu  
 50 55 60  
 Lys Ser Leu Pro Glu Val Gly Glu Ala Asp Val Glu Gly Glu Val Lys  
 65 70 75 80  
 Lys Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Arg  
 85 90 95  
 Glu Glu Glu His Ala Lys Leu Met Lys Ala Leu Lys Lys Lys Lys Lys  
 100 105 110

<210> 118  
 <211> 56  
 <212> PRT  
 <213> Rattus

<400> 118  
 Thr Asp Ala Thr Asp Gly Asn Leu Lys Ser Leu Pro Glu Val Gly Glu  
 1 5 10 15  
 Ala Asp Val Glu Gly Glu Val Lys Lys Ala Leu Ile Gly Ile Lys Gln  
 20 25 30  
 Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ala Lys Leu Met  
 35 40 45

Lys Ala Leu Lys Lys Lys Lys Lys  
50 55

<210> 119  
<211> 1545  
<212> DNA  
<213> Rattus

<400> 119  
ggcaccgagg cacatcgtaa aaagtgaagg tcctttcaga agttagtggc aattttctctg 60  
gggagagctg caatatcggt ggaacactgg accatgcagc caccactctt tgtgatttct 120  
gtgtatctgt tatggtgaaa tattgtgaca gtgcacctac ttggaaggag acagatgcta 180  
cggatggaaa cctaaagagt cttccagagg taggagagggc agatgtagag ggagaggtca 240  
agaaggcttt gattggcatt aagcaaataa aaatcatgat ggaaaggaga gaggaggaaac 300  
acgcaaaatt gatgaaagcc ttgaagaagt gcaaagaaga aaagcaggag gccagaaac 360  
tcatgaacga agtgcaagaa cgtctggagg aagaagaaaa gctatgtcag gcatcttcta 420  
taggttcttg ggatggatgc aggccatgtt tggaaagtaa ctgcatacga tttatacacg 480  
cttgccaacc tggttggtcc tctgtgaaaa gcatgatgaa gcaatttctc aagaagatat 540  
accgatttct gtcttccag agtgaagatg taaaggatcc ccctgccata gaacagctga 600  
ctaaggaaga tttacaagtg gtacacatag agaacctgtt tagccagctg gccgtggatg 660  
caaaatctct cttcaacatg agcttttaca tttttaagca gatgcagcaa gaatttgatc 720  
aggcttttca attatacttc atgtccgatg tggacttaat ggagccatac cccccagctt 780  
tatctaaaga gataatcaaa aaagaagaac ttggggcaaa gtggggcatt cccaatgtct 840  
tccagctgtt tcataatttc agtctctctg tttatgggag agtccaacaa ataataatga 900  
agacactcaa tgcaattgaa gattcatggg aaccacacaa agagttagac cagagaggta 960  
tgacttcaga gatgttacct gagcaaaatg gagaaatgtg tgaggaattt gtcaagaatt 1020  
tatctggatg tttaaaattt cgtaaaagat gccaaaaatg tcacaattac ctatctgaag 1080  
aatgccctga tgtacctgaa cttcacatag aattccttga ggccctgaaa ttagtcaatg 1140  
tatccaatca gcaatatgat cagattgtcc agatgaccca gtatcatttg gaagatacca 1200  
tatacctgat ggagaaaatg caagagcagt ttggatgggt gtctcaactg gcaagccata 1260  
accagtgac tgaggacatc ttttaattcaa caaaggcagt tccaaagatt catggaggag 1320  
attcttccaa gcaggatgaa attatggtag actcaagcag cattctgcct tcctctaact 1380  
tcaccgtcca gaatcctcct gaagaagggtg ctgagagctc aaatgttatt tactacatgg 1440  
cagctaaagt tctgcagcat ctaaagggat gttttgaaac ttggttaagaa tagctgatta 1500  
ggaaagcttt gttgagaggg taggtaacat aaaaaaaaaa aaaaa 1545

<210> 120  
<211> 512  
<212> PRT  
<213> Rattus

<400> 120  
His Arg Gly Thr Ser Glx Lys Val Lys Val Leu Ser Glu Val Ser Gly  
1 5 10 15  
Asn Phe Ser Gly Glu Ser Cys Asn Ile Gly Gly Thr Leu Asp His Ala  
20 25 30  
Ala Thr Thr Leu Cys Asp Phe Cys Val Ser Val Met Val Lys Tyr Cys  
35 40 45  
Asp Ser Ala Pro Thr Trp Lys Glu Thr Asp Ala Thr Asp Gly Asn Leu  
50 55 60  
Lys Ser Leu Pro Glu Val Gly Glu Ala Asp Val Glu Gly Glu Val Lys  
65 70 75 80  
Lys Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Arg  
85 90 95  
Glu Glu Glu His Ala Lys Leu Met Lys Ala Leu Lys Lys Cys Lys Glu  
100 105 110  
Glu Lys Gln Glu Ala Gln Lys Leu Met Asn Glu Val Gln Glu Arg Leu  
115 120 125  
Glu Glu Glu Glu Lys Leu Cys Gln Ala Ser Ser Ile Gly Ser Trp Asp  
130 135 140  
Gly Cys Arg Pro Cys Leu Glu Ser Asn Cys Ile Arg Phe Tyr Thr Ala  
145 150 155 160

Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	Phe	Leu	
				165					170					175		
Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	Lys	Asp	
			180					185					190			
Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	Val	His	
		195					200					205				
Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	Leu	Phe	
	210					215					220					
Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln	
225					230					235					240	
Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	Pro	Tyr	
			245						250					255		
Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu	Gly	Gln	
			260					265					270			
Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	Ser	Leu	
		275					280					285				
Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	Asn	Ala	
	290					295					300					
Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	Gly	Met	
305					310					315					320	
Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	Glu	Phe	
				325					330						335	
Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	Gln	Lys	
			340					345					350			
Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	Leu	His	
		355					360					365				
Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	Gln	Gln	
	370					375					380					
Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	Thr	Ile	
385					390					395					400	
Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	Gln	Leu	
			405						410					415		
Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys	Ala	
			420					425					430			
Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu	Ile	Met	
		435					440					445				
Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val	Gln	Asn	
	450					455					460					
Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr	Met	Ala	
465					470					475					480	
Ala	Lys	Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp	Glu	Leu	
			485						490					495		
Ile	Arg	Lys	Ala	Leu	Leu	Arg	Gly	Asn	Val	Thr	Asn	Lys	Lys	Lys	Lys	
			500					505					510			

<210> 121  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<400> 121	
gaattagacg aggcgatcag gttgggtcaat gtatccaatc agcagtatgg ccagattctc	60
cagatgaccc ggaagcactt ggaggacacc gcctatctgg tggagaagat gagagggcaa	120
tttggctggg tgtctgaact ggcaaaccag gccccagaaa cagagatcat cttaattca	180
atacaggtaa gaagatctaa tgcatcctat atccagtaag t	221

<210> 122  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

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<400> 122
acacagaatt agacgaggcg atcagggttg tcaatgtatc caatcagcag tatggccaga      60
ttctccagat gacccggaag cacttggagg acaccgccta tctgggtggag aagatgagag      120
ggcaatttgg ctgggtgtct gaactggcaa accaggcccc agaaacagag atcatcttta      180
attcaataca ggtagttcca aggattcatg aaggaaatat ttccaaacaa gatgaaacaa      240
tgatgacaga cttaaagcatt ctgccttcct ctaatttcac actcaagatc cctcttgaag      300
aaagtgtctg gagtttctaac ttcatgtggt acgtagtggc aaaagctcta cagcatttta      360
aggaacattt taaaacctgg taagcagagt gcctggttag gaatgccttg ttgacaggaa      420
tagttaattc tcaaaaggga aaaacaaaac ttgtttcaaa atacctggaa aacatgttta      480
acctcattaa taaagacatg aaaacaaaac agatggcatt ttct                                524

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<210> 123
<211> 568
<212> DNA
<213> Homo sapiens

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<400> 123
gaattagacg aggcgatcag gttgggtcaat gtatccaatc agcagtatgg ccagattctc      60
cagatgaccc ggaagcactt ggaggacacc gcctatctgg tggagaagat gagagggcaa      120
tttggtctgg tgtctgaact ggcaaaccag gcccagaaa cagagatcat ctttaattca      180
atacaggtag ttccaaggat tcatgaagga aatatttcca aacaagatga aacaatgatg      240
acagacttaa gcattctgcc ttctctaat ttcacactca agatccctct tgaagaaagt      300
gctgagagtt ctaacttcat tggctacgta gtggcaaaaag ctctacagca ttttaaggaa      360
cattttaaaa cctgaaaaaag atcctgaggc tcagtgtcca aggtccaatg aactactcag      420
gtcggagggtg gtagagcagc atgtggagcc agttctctct ccgactccat catcacactg      480
cacggttcc tgtaagata tttgtcaaa aaatgcgaga tataaaaatc tgggtaagaa      540
gatctaattg atcctatatc cagtaagt                                568

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<210> 124
<211> 1141
<212> DNA
<213> H. sapiens

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<220>
<221> misc feature
<222> (789)...(798)
<223> additional sequence present in full genomic sequence

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<400> 124
cctgaaagcc tggcgccaat gacccgcgag acattttttg cctgggggtgc tcctgtcgga      60
aaggaaagag gaaaggacga ctaagaactt atactcgaac tcccgaattt ctcttttcaa      120
ggtttaagag gaaagctggt tcgtggggat tggatgggag gccaccagga aaccaagttc      180
ccgcgccagc ttcagtgtct tcctcttycc gcgcctttg ccccgccac atcactttcg      240
ctccagtttt tgaaaacgct gcgaagcgga atggtccaca ggggaaaacg gaggaggggc      300
caaagccagg actttgagac cggcgcgcgg tcaagccag gcagctctcc ctaaccctcc      360
agcactgggc aaacgctgcc cgatgacgcc cgctcgggg gccacggcat cactggggcg      420
actgcgagcc cggcgcgga gccgctggga cgcggttac ctcccggtg tcgctgctgt      480
gtgtgttgcc cgcgccagtc acgtccctaa tgggaccctc cgtttcggcg tctgtaaggc      540
gaggaggacg atgcgtcccc tccctsgcag gattgaggtt aggactaaac ggggtccgca      600
gcgcccggca gctcccagc gctctcccca gcgcgcctc cctccttccc gccaccgctc      660
ccgcaggggc ccgcggcgct acctctcagg ctgtagcgcg cctgcatgcc gaataccgac      720
agggtgccgg tgcctgtgct gtcgtccttc ctgacgcgc agcggaggat gtgttgatc      780
tgccccaggt actttcagga ttccaggctc ccagatgaag agataattct acttactgga      840
tataggatgc attagatctt cttaccttaa aaaaaaaaaa aaaggcagca atgatcaaaa      900
tactaataaa ttactcacag actcagtgtt tttttcttg gagtaaaagt ccaggatggg      960
taatagaata cctgctgttg gcttttgga aaattggtac tgtatgtagc aaaataatgt      1020
gaaaccata tgcattgata ttcttaacaa tttgaagaaa tcgtcacagc tttcctgggt      1080
tgttgagcct ctaaaatggt ctttctctct gatgtgataa taaagtgttt attttgaact      1140
c                                                                1141

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<210> 125
<211> 27

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<212> PRT  
<213> Homo sapiens

<400> 125  
Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys Leu  
1 5 10 15  
Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys  
20 25

<210> 126  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 126  
Gly Glu Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys  
1 5 10 15  
Cys Gln Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro  
20 25

<210> 127  
<211> 27  
<212> PRT  
<213> Cavia sp.

<400> 127  
Cys Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu  
1 5 10 15  
Glu Ser Asn Cys Met Arg Phe Asp Thr Thr Cys  
20 25

<210> 128  
<211> 30  
<212> PRT  
<213> Cavia sp.

<400> 128  
Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp Cys Val Asn Phe Arg Lys  
1 5 10 15  
Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser Asp Asp Cys Pro  
20 25 30

<210> 129  
<211> 27  
<212> PRT  
<213> Bos sp.

<400> 129  
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Glu Ser Asp Cys Met Arg Phe Tyr Thr Thr Cys  
20 25

<210> 130  
<211> 29  
<212> PRT  
<213> Bos sp.

<400> 130  
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1 5 10 15  
Ala Arg Cys Gln Lys Cys Gln Asp Tyr Leu Trp Ala Asp

<210> 131  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<400> 131  
 Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys Leu  
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<210> 132  
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 <212> PRT  
 <213> Homo sapiens

<400> 132  
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<210> 133  
 <211> 494  
 <212> PRT  
 <213> Homo sapiens

<400> 133  
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 Gln Leu His Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro  
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 Pro Leu Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His  
 35 40 45  
 Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys  
 50 55 60  
 Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys  
 65 70 75 80  
 Ala Leu Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu  
 85 90 95  
 Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu  
 100 105 110  
 Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu  
 115 120 125  
 Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu  
 130 135 140  
 Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys  
 145 150 155 160  
 Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg  
 165 170 175  
 Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp  
 180 185 190  
 Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln  
 195 200 205  
 Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe  
 210 215 220  
 Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln  
 225 230 235 240  
 Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr  
 245 250 255  
 Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu  
 260 265 270

Gln	Cys	Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn	Phe	Ser	
	275						280					285				
Val	Ser	Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	Leu	Lys	
	290					295					300					
Ala	Ile	Glu	Asp	Leu	Pro	Lys	Gln	Asp	Lys	Ala	Pro	Asp	His	Gly	Gly	
305					310					315					320	
Leu	Ile	Ser	Lys	Met	Leu	Pro	Gly	Gln	Asp	Arg	Gly	Leu	Cys	Gly	Glu	
			325					330						335		
Leu	Asp	Gln	Asn	Leu	Ser	Arg	Cys	Phe	Lys	Phe	His	Glu	Lys	Cys	Gln	
		340					345					350				
Lys	Cys	Gln	Ala	His	Leu	Ser	Glu	Asp	Cys	Pro	Asp	Val	Pro	Ala	Leu	
	355					360						365				
His	Thr	Glu	Leu	Asp	Glu	Ala	Ile	Arg	Leu	Val	Asn	Val	Ser	Asn	Gln	
	370					375					380					
Gln	Tyr	Gly	Gln	Ile	Leu	Gln	Met	Thr	Arg	Lys	His	Leu	Glu	Asp	Thr	
385					390					395					400	
Ala	Tyr	Leu	Val	Glu	Lys	Met	Arg	Gly	Gln	Phe	Gly	Trp	Val	Ser	Glu	
			405					410					415			
Leu	Ala	Asn	Gln	Ala	Pro	Glu	Thr	Glu	Ile	Ile	Phe	Asn	Ser	Ile	Gln	
		420					425					430				
Val	Val	Pro	Arg	Ile	His	Glu	Gly	Asn	Ile	Ser	Lys	Gln	Asp	Glu	Thr	
	435					440					445					
Met	Met	Thr	Asp	Leu	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Leu	Lys	
	450				455						460					
Ile	Pro	Leu	Glu	Glu	Ser	Ala	Glu	Ser	Ser	Asn	Phe	Ile	Gly	Tyr	Val	
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Val	Ala	Lys	Ala	Leu	Gln	His	Phe	Lys	Glu	His	Phe	Lys	Thr			
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<210> 134  
 <211> 1541  
 <212> DNA  
 <213> Rattus

<400> 134

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actctttgtg	atctctgtgt	atctgttatg	gttgaaatat	tgtgacagtg	cacctacttg	180
gaaggagaca	gatgctacgg	atggaaacct	aaagagtctt	ccagaggtag	gagaggcaga	240
tgtagaggga	gaggtcaaga	aggctttgat	tggcattaag	caaataaaaa	tcatgatgga	300
aaggagagag	gaggaacacg	caaaattgat	gaaagccttg	aagaagtgca	aagaagaaaa	360
gcaggaggcc	cagaaaactca	tgaacgaagt	gcaagaacgt	ctggaggaag	aagaaaagct	420
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gcagcaagaa	tttgatcagg	cttttcaatt	atacttcatt	tccgatgtgg	acttaatgga	780
gccatacccc	ccagctttat	ctaaagagat	aatcaaaaaa	gaagaacttg	ggcaaagggtg	840
gggcattccc	aatgtcttcc	agctgtttca	taatttcagt	ctctctgttt	atgggagagt	900
ccaacaaata	ataatgaaga	cactcaatgc	aattgaagat	tcatgggaac	cacacaaaga	960
gtagaccag	agaggtatga	cttcagagat	gttacctgag	caaaatggag	aaatgtgtga	1020
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caattacctt	tctgaagaat	gccctgatgt	acctgaactt	cacatagaat	tccttgaggc	1140
cctgaaatta	gtcaatgtat	ccaatcagca	atatgatcag	attgtccaga	tgaccagta	1200
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tcaactggca	agccataacc	cagtgactga	ggacatcttt	aattcaacaa	aggcagttcc	1320
aaagattcat	ggaggagatt	cttccaagca	ggatgaaatt	atggtagact	caagcagcat	1380
tctgccttcc	tctaacttca	ccgtccagaa	tcctcctgaa	gaaggtgctg	agagctcaaa	1440
tgttattttac	tacatggcag	ctaaagttct	gcagcatcta	aagggtgtgt	ttgaaacttg	1500
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<210> 135  
 <211> 464  
 <212> PRT  
 <213> Rattus

<400> 135

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			20					25					30		
Asn	Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu
		35					40					45			
Val	Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
	50					55					60				
Arg	Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys
65					70					75					80
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu
				85					90					95	
Arg	Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser
				100				105					110		
Trp	Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr
	115						120					125			
Thr	Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln
	130					135						140			
Phe	Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val
145					150					155					160
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val
				165					170					175	
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser
			180					185					190		
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe
	195						200					205			
Asp	Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu
	210					215					220				
Pro	Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu
225					230					235					240
Gly	Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe
				245					250					255	
Ser	Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu
			260					265					270		
Asn	Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg
	275						280					285			
Gly	Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu
	290					295					300				
Glu	Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys
305					310					315					320
Gln	Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu
				325					330					335	
Leu	His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn
			340					345					350		
Gln	Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp
		355					360					365			
Thr	Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser
	370					375					380				
Gln	Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr
385					390					395					400
Lys	Ala	Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu
				405					410					415	
Ile	Met	Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val
			420					425					430		
Gln	Asn	Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr

435 440 445  
Met Ala Ala Lys Val Leu Gln His Leu Lys Gly Cys Phe Glu Thr Trp  
450 455 460

<210> 136  
<211> 1541  
<212> DNA  
<213> Rattus

<400> 136  
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actctttgtg atttctgtgt atctgttatg gttgaaatat tgtgacagtg cacctacttg 180  
gaaggagaca gatgctacgg atggaaacct aaagagtctt ccagaggtag gagaggcaga 240  
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aaggagagag gaggaacacg caaaattgat gaaagccttg aagaagtgca aagaagaaaa 360  
gcaggaggcc cagaaactca tgaacgaagt gcaagaacgt ctggagggaag aagaaaagct 420  
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tgccatagaa cagctgacta aggaagattt acaagtggta cacatagaga acctgttttag 660  
ccagctggcc gtggatgcaa aatctctctt caacatgagc ttttacattt ttaagcagat 720  
gcagcaagaa tttgatcagg cttttcaatt atacttcatg tccgatgtgg acttaatgga 780  
gccatacccc ccagctttat cttaaagagat aatcaaaaaa gaagaacttg ggcaaagggtg 840  
gggcattccc aatgtcttcc agctgtttca taatttcagt ctctctgttt atgggagagt 900  
ccaacaaata ataatgaaga cactcaatgc aattgaagat tcatgggaac cacacaaaga 960  
gtagaccag agaggtatga cttcagagat gttacctgag caaaatggag aaatgtgtga 1020  
ggaatttgtc aagaatttat ctggatgttt aaaatttcgt aaaagatgcc aaaaatgtca 1080  
caattaccta tctgaagaat gccctgatgt acctgaactt cacatagaat tccttgaggc 1140  
cctgaaatta gtcaatgtat ccaatcagca atatgatcag attgtccaga tgaccagta 1200  
tcatttggaa gataccatat acctgatgga gaaaatgcaa gagcagtttg gatgggtgtc 1260  
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aaagattcat ggaggagatt cttccaagca ggatgaaatt atggtagact caagcagcat 1380  
tctgccttcc tctaacttca ccgtccagaa tcctcctgaa gaagggtgtg agagctcaaa 1440  
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<210> 137  
<211> 464  
<212> PRT  
<213> Rattus

<400> 137  
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Tyr Cys Asp Ser Ala Pro Thr Trp Lys Glu Thr Asp Ala Thr Asp Gly  
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Asn Leu Lys Ser Leu Pro Glu Val Gly Glu Ala Asp Val Glu Gly Glu  
35 40 45  
Val Lys Lys Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu  
50 55 60  
Arg Arg Glu Glu Glu His Ala Lys Leu Met Lys Ala Leu Lys Lys Cys  
65 70 75 80  
Lys Glu Glu Lys Gln Glu Ala Gln Lys Leu Met Asn Glu Val Gln Glu  
85 90 95  
Arg Leu Glu Glu Glu Glu Lys Leu Cys Gln Ala Ser Ser Ile Gly Ser  
100 105 110  
Trp Asp Gly Cys Arg Pro Cys Leu Glu Ser Asn Cys Ile Arg Phe Tyr  
115 120 125  
Thr Ala Cys Gln Pro Gly Trp Ser Ser Val Lys Ser Met Met Lys Gln  
130 135 140  
Phe Leu Lys Lys Ile Tyr Arg Phe Leu Ser Ser Gln Ser Glu Asp Val

145		150		155		160									
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val
		165		170		175									
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser
		180		185		190									
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe
		195		200		205									
Asp	Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu
		210		215		220									
Pro	Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Thr	Lys	Lys	Glu	Glu	Leu
		225		230		235									
Gly	Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe
		245		250		255									
Ser	Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu
		260		265		270									
Asn	Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg
		275		280		285									
Gly	Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu
		290		295		300									
Glu	Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys
		305		310		315									
Gln	Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu
		325		330		335									
Leu	His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn
		340		345		350									
Gln	Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp
		355		360		365									
Thr	Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser
		370		375		380									
Gln	Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr
		385		390		395									
Lys	Ala	Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu
		405		410		415									
Ile	Met	Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val
		420		425		430									
Gln	Asn	Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr
		435		440		445									
Met	Ala	Ala	Lys	Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp
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<210> 138  
 <211> 1326  
 <212> DNA  
 <213> Rattus

<400> 138	
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gaaggagaca gatgctacgg atggaaacct aaagagtctt ccagaggtag gagaggcaga	240
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aaggagagag gaggaacacg caaaattgat gaaagccttg aagaagtgca aagaagaaaa	360
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catacgattt tatacagctt gccaacctgg ttggtcctct gtgaaaagca tgatgaagca	540
atttctcaag aagatatacc gatttctgtc ttcccagagt gaagatgtaa aggatcccc	600
tgccatagaa cagctgacta aggaagattt acaagtggta cacatagaga acctgtttag	660
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gcagcaagaa tttgatcagg cttttcaatt atacttcatg tccgatgtgg acttaatgga	780
gccatacccc ccagctttat cttaaagagat aacaaaaaaa gaagaacttg ggcaaagggtg	840
gggcattccc aatgtcttcc agctgtttca taatttcagt ctctctgttt atgggagagt	900
ccaacaaata ataatgaaga cactcaatgc aattgaagat tcatgggaac cacacaaaga	960

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ggaatttgtc	aagaatttat	ctggatgttt	aaaatttcgt	aaaagatgcc	aaaaatgtca	1080
caattaccta	tctgaaggca	gttccaaaga	ttcatggagg	agattcttcc	aagcaggatg	1140
aaattatggt	agactcaagc	agcattctgc	cttcctctaa	cttcaccgtc	cagaatcctc	1200
ctgaagaagg	tgctgagagc	tcaaagtgtta	tttactacat	ggcagctaaa	gttctgcagc	1260
atctaaaggg	atgttttgaa	acttggttaag	aatagctgat	taggaaagct	ttgttgagag	1320
ggtagg						1326

<210> 139

<211> 344

<212> PRT

<213> Rattus

<400> 139

Met	Gln	Pro	Pro	Leu	Phe	Val	Ile	Ser	Val	Tyr	Leu	Leu	Trp	Leu	Lys	
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Tyr	Cys	Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly	
			20					25					30			
Asn	Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu	
		35					40					45				
Val	Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	
	50					55					60					
Arg	Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys	
65					70					75					80	
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu	
				85					90					95		
Arg	Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser	
			100					105					110			
Trp	Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr	
		115					120					125				
Thr	Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	
	130					135					140					
Phe	Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	
145				150						155					160	
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	
				165				170						175		
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	
			180				185					190				
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	
	195					200					205					
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<400> 141

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<210> 145  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

Lys	Pro	Gly	Asp	Phe	Ile	His	Thr	Leu	Gly	Asp	Ala	His	Ile	Tyr	Leu		
1				5					10					15			
Asn	His	Ile	Glu	Pro	Leu	Lys	Ile	Gln	Leu	Gln	Arg	Glu	Pro	Arg	Pro		
			20					25					30				
Phe	Pro	Lys	Leu	Arg	Ile	Leu	Arg	Lys	Val	Glu	Lys	Ile	Asp	Asp	Phe		
		35					40					45					
Lys	Ala	Glu	Asp	Phe	Gln	Ile	Glu	Gly	Tyr	Asn	Pro	His	Pro	Thr	Ile		
50						55					60						
Lys	Met	Glu	Met	Ala	Val												
65					70												

<210> 146  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

Leu	Pro	Leu	Met	Ala	Leu	Pro	Pro	Cys	His	Ala	Leu	Cys	Gln	Phe	Tyr		
1				5					10					15			
Val	Val																

<210> 147  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

Met	Gly	Leu	Gly	Val	Pro	Phe	Asn	Ile	Ala	Ser	Tyr	Ala	Leu	Leu	Thr		
1				5					10					15			
Tyr	Met	Ile	Ala	His	Ile	Thr	Gly	Leu									
			20					25									

<210> 148  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 148

Asn Ser Glu Leu Ser Cys Gln Leu Tyr Gln Arg Ser Gly Asp  
1 5 10

<210> 149

<211> 14

<212> PRT

<213> Homo sapiens

<400> 149

Asn Ser Glu Leu Ser Cys Gln Leu Tyr Gln Arg Ser Gly Asp  
1 5 10

<210> 150

<211> 18

<212> PRT

<213> Homo sapiens

<400> 150

Leu Pro Leu Met Ala Leu Pro Pro Cys His Ala Leu Cys Gln Phe Tyr  
1 5 10 15  
Val Val

<210> 151

<211> 25

<212> PRT

<213> Homo sapiens

<400> 151

Met Gly Leu Gly Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr  
1 5 10 15  
Tyr Met Ile Ala His Ile Thr Gly Leu  
20 25

<210> 152

<211> 186

<212> PRT

<213> Homo sapiens

<400> 152

Met Pro Val Ala Gly Ser Glu Leu Pro Arg Arg Pro Leu Pro Pro Ala  
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Ala Gln Glu Arg Asp Ala Glu Pro Arg Pro Pro His Gly Glu Leu Gln  
20 25 30  
Tyr Leu Gly Gln Ile Gln His Ile Leu Arg Cys Gly Val Arg Lys Asp  
35 40 45  
Asp Arg Thr Gly Thr Gly Thr Leu Ser Val Phe Gly Met Gln Ala Arg  
50 55 60  
Tyr Ser Leu Arg Asp Glu Phe Pro Leu Leu Thr Thr Lys Arg Val Phe  
65 70 75 80  
Trp Lys Gly Val Leu Glu Glu Leu Leu Trp Phe Ile Lys Gly Ser Thr  
85 90 95  
Asn Ala Lys Glu Leu Ser Ser Lys Gly Val Lys Ile Trp Asp Ala Asn  
100 105 110  
Gly Ser Arg Asp Phe Leu Asp Ser Leu Gly Phe Ser Thr Arg Glu Glu  
115 120 125  
Gly Asp Leu Gly Pro Val Tyr Gly Phe Gln Trp Arg His Phe Gly Ala  
130 135 140

Glu Tyr Arg Asp Met Glu Ser Asp Tyr Ser Gly Gln Gly Val Asp Gln  
 145 150 155 160  
 Leu Gln Arg Val Ile Asp Thr Ile Lys Thr Asn Pro Asp Asp Arg Arg  
 165 170 175  
 Ile Ile Met Cys Ala Trp Asn Pro Arg Asp  
 180 185

<210> 153  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
 Lys Pro Gly Asp Phe Ile His Thr Leu Gly Asp Ala His Ile Tyr Leu  
 1 5 10 15  
 Asn His Ile Glu Pro Leu Lys Ile Gln Leu Gln Arg Glu Pro Arg Pro  
 20 25 30  
 Phe Pro Lys Leu Arg Ile Leu Arg Lys Val Glu Lys Ile Asp Asp Phe  
 35 40 45  
 Lys Ala Glu Asp Phe Gln Ile Glu Gly Tyr Asn Pro His Pro Thr Ile  
 50 55 60  
 Lys Met Glu Met Ala Val  
 65 70

<210> 154  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<400> 154  
 gtcattgcttt tatacattct ggc 23

<210> 155  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 155  
 ttattctgttt agatcagcac tacac 25

<210> 156  
 <211> 28  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 gtacttgata tttatataca tcctaatac 28

<210> 157  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 gtaatccaac actttgggag g 21

<210> 158  
 <211> 70  
 <212> PRT

<213> Homo sapiens

<400> 158

Lys	Pro	Gly	Asp	Phe	Ile	His	Thr	Leu	Gly	Asp	Ala	His	Ile	Tyr	Leu
1				5					10					15	
Asn	His	Ile	Glu	Pro	Leu	Lys	Ile	Gln	Leu	Gln	Arg	Glu	Pro	Arg	Pro
			20					25					30		
Phe	Pro	Lys	Leu	Arg	Ile	Leu	Arg	Lys	Val	Glu	Lys	Ile	Asp	Asp	Phe
		35				40						45			
Lys	Ala	Glu	Asp	Phe	Gln	Ile	Glu	Gly	Tyr	Asn	Pro	His	Pro	Thr	Ile
	50					55					60				
Lys	Met	Glu	Met	Ala	Val										
65					70										

<210> 159

<211> 437

<212> PRT

<213> H. sapiens

<400> 159

Met	Lys	Ile	Lys	Ala	Glu	Lys	Asn	Glu	Gly	Pro	Ser	Arg	Ser	Trp	Trp
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Gln	Leu	His	Trp	Gly	Asp	Ile	Ala	Asn	Asn	Ser	Gly	Asn	Met	Lys	Pro
			20					25					30		
Pro	Leu	Leu	Val	Phe	Ile	Val	Cys	Leu	Leu	Trp	Leu	Lys	Asp	Ser	His
		35				40						45			
Cys	Ala	Pro	Thr	Trp	Lys	Asp	Lys	Thr	Ala	Ile	Ser	Glu	Asn	Leu	Lys
	50					55					60				
Ser	Phe	Ser	Glu	Val	Gly	Glu	Ile	Asp	Ala	Asp	Glu	Glu	Val	Lys	Lys
65					70				75					80	
Ala	Leu	Thr	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	Lys	Glu
			85						90					95	
Lys	Glu	His	Thr	Asn	Leu	Met	Ser	Thr	Leu	Lys	Lys	Cys	Arg	Glu	Glu
		100						105					110		
Lys	Gln	Glu	Ala	Leu	Lys	Leu	Leu	Asn	Glu	Val	Gln	Glu	His	Leu	Glu
		115					120					125			
Glu	Glu	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser	Trp	Gly	Glu
	130					135					140				
Cys	Arg	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr	Thr	Thr	Cys
145					150					155					160
Gln	Pro	Ser	Trp	Ser	Ser	Val	Lys	Asn	Lys	Ile	Glu	Arg	Phe	Phe	Arg
			165						170					175	
Lys	Ile	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	Lys	Asp
		180						185					190		
Leu	Pro	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	Thr	Gln
	195					200						205			
Met	Glu	Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser	Leu	Phe
	210					215					220				
Asn	Arg	Ser	Phe	Asn	Val	Phe	Arg	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln
225					230					235					240
Thr	Phe	Gln	Ser	His	Phe	Ile	Ser	Asp	Thr	Asp	Leu	Thr	Glu	Pro	Tyr
			245						250					255	
Phe	Phe	Pro	Ala	Phe	Ser	Lys	Glu	Pro	Met	Thr	Lys	Ala	Asp	Leu	Glu
		260						265					270		
Gln	Cys	Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn	Phe	Ser
	275					280						285			
Val	Ser	Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	Leu	Lys
	290					295					300				
Ala	Ile	Glu	Asp	Leu	Pro	Lys	Gln	Asp	Lys	Ala	Pro	Asp	His	Gly	Gly
305					310					315					320
Leu	Ile	Ser	Lys	Met	Leu	Pro	Gly	Gln	Asp	Arg	Gly	Leu	Cys	Gly	Glu
				325					330					335	

Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln  
                   340                  345                  350  
 Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu  
                   355                  360                  365  
 His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln  
                   370                  375                  380  
 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr  
                   385                  390                  395                  400  
 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu  
                   405                  410                  415  
 Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Arg Arg Ser Asn  
                   420                  425                  430  
 Ala Ser Tyr Ile Gln  
                   435

<210> 160  
 <211> 1134  
 <212> DNA  
 <213> H. sapiens

<400> 160  
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 agaggaaagc tggttcgtgg ggattggatg ggaggccacc aggaaaccaa gttcccgcgc 180  
 cagcttcagt gctstcctct tcccgcgcgc tttgccccgc ccacatcact ttcgctccag 240  
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<210> 161  
 <211> 50  
 <212> PRT  
 <213> H. sapien

<220>  
 <221> misc\_feature  
 <222> (45)...(45)  
 <223> Xaa = Ile or Leu

<400> 161  
 Phe Gly Trp Val Ser Glu Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile  
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 Ile Phe Asn Ser Ile Gln Val Val Pro Arg Ile His Glu Gly Asn Ile  
                   20                  25                  30  
 Ser Lys Gln Asp Glu Thr Met Met Thr Asp Leu Ser Xaa Pro Ser Ser  
                   35                  40                  45  
 Asn Phe  
   50

<210> 162

<211> 49  
 <212> PRT  
 <213> bovine  
  
 <220>  
 <221> misc\_feature  
 <222> (44)...(44)  
 <223> Xaa = Ile or Leu  
  
 <400> 162  
 Phe Gly Trp Val Thr Glu Leu Ala Ser Gln Thr Pro Gly Ser Glu Asn  
 1 5 10 15  
 Ile Phe Ser Phe Ile Lys Val Val Pro Gly Val His Glu Gly Asn Phe  
 20 25 30  
 Ser Lys Gln Asp Glu Lys Met Ile Asp Ile Ser Xaa Pro Ser Ser Asn  
 35 40 45  
 Phe  
  
 <210> 163  
 <211> 51  
 <212> PRT  
 <213> guinea pig  
  
 <220>  
 <221> misc\_feature  
 <222> (46)...(46)  
 <223> Xaa = Ile or Leu  
  
 <400> 163  
 Phe Gly Trp Val Leu Glu Leu Ala Tyr Gln Ser Pro Gly Ala Glu Asp  
 1 5 10 15  
 Ile Phe Asn Pro Val Lys Val Met Val Ala Leu Ser Ala His Glu Gly  
 20 25 30  
 Asn Ser Ser Asp Gln Asp Asp Thr Val Val Pro Ser Ser Xaa Pro Ser  
 35 40 45  
 Ser Asn Phe  
 50  
  
 <210> 164  
 <211> 49  
 <212> PRT  
 <213> rat  
  
 <220>  
 <221> misc\_feature  
 <222> (44)...(44)  
 <223> Xaa = Ile or Leu  
  
 <400> 164  
 Phe Gly Trp Val Ser Gln Leu Ala Ser His Asn Pro Val Thr Glu Asp  
 1 5 10 15  
 Ile Phe Asn Ser Thr Lys Ala Val Pro Lys Ile His Gly Gly Asp Ser  
 20 25 30  
 Ser Lys Gln Asp Glu Ile Met Val Asp Ser Ser Xaa Pro Ser Ser Asn  
 35 40 45  
 Phe  
  
 <210> 165  
 <211> 1767  
 <212> DNA  
 <213> Cavia sp.

<400> 165

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actgcaagga	ttaacagtga	gaacatgaag	ctgccacttt	tgatgtttcc	cgtgtgtctg	180
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aacgcgaaca	gtttttctga	ggctggggag	atagacgtag	atggagaggt	gaagatagct	300
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